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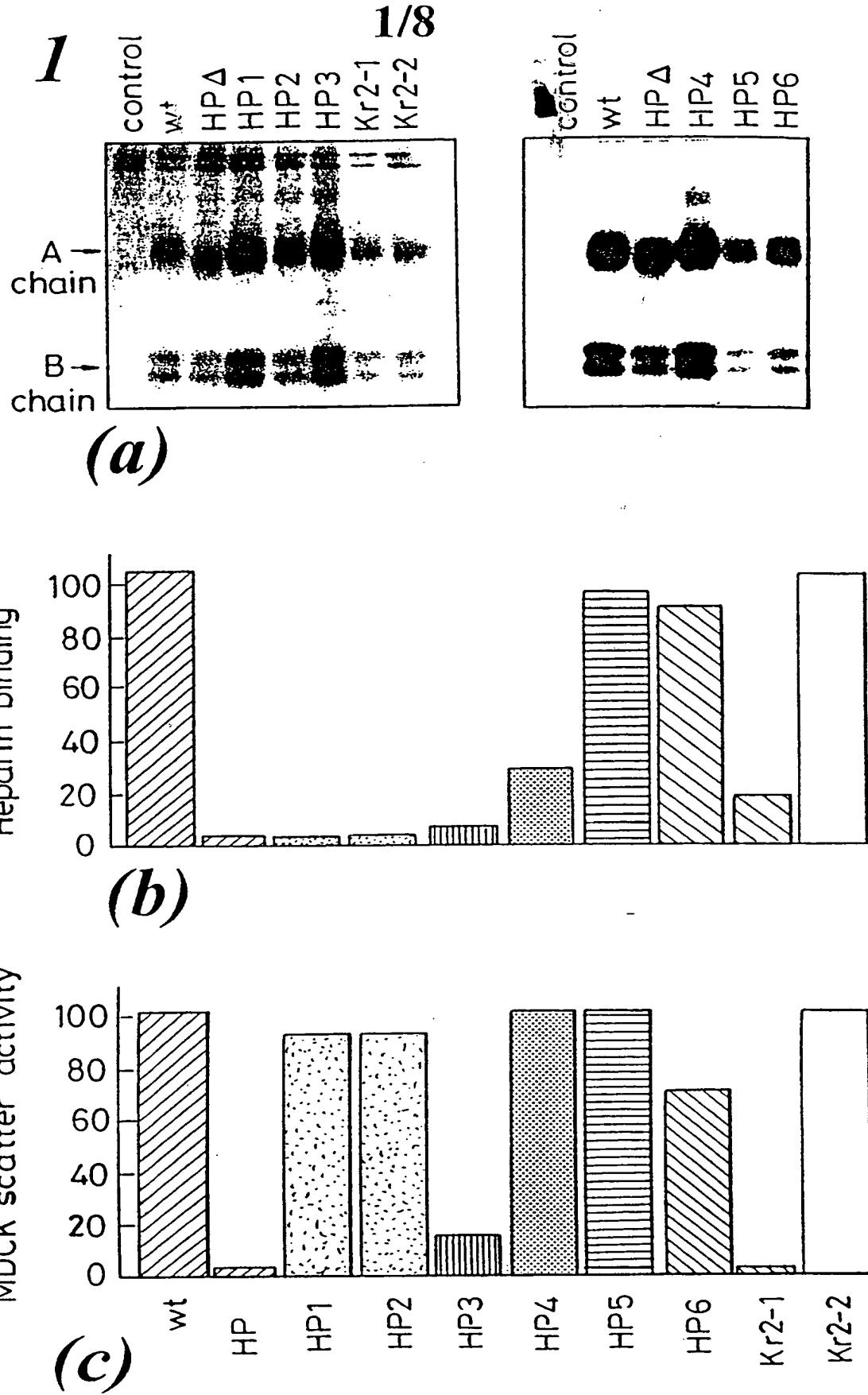
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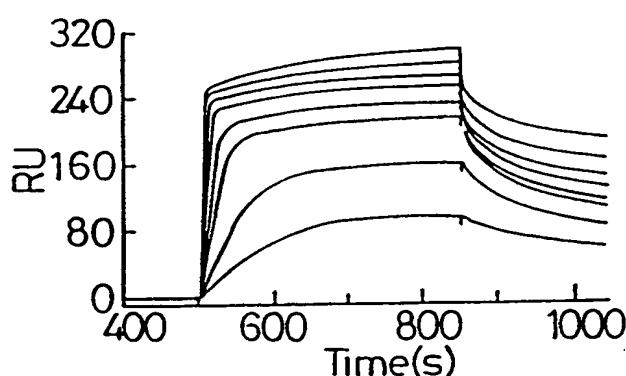
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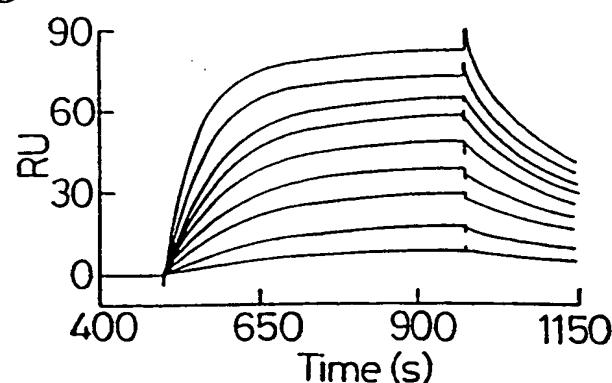
Fig 1



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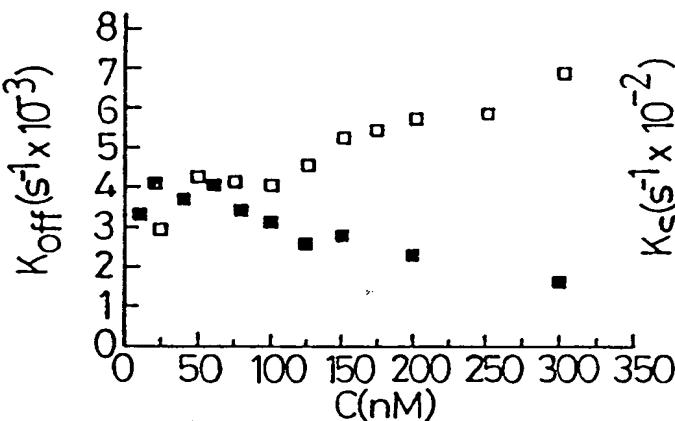


(a)

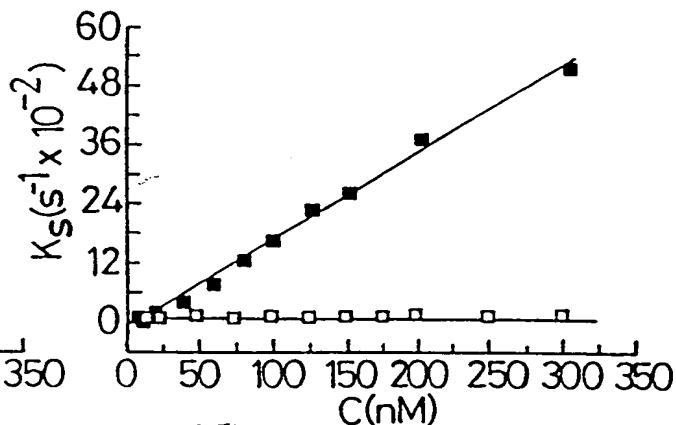


(b)

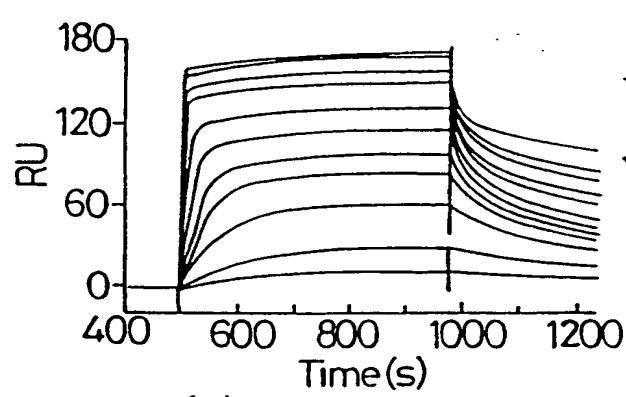
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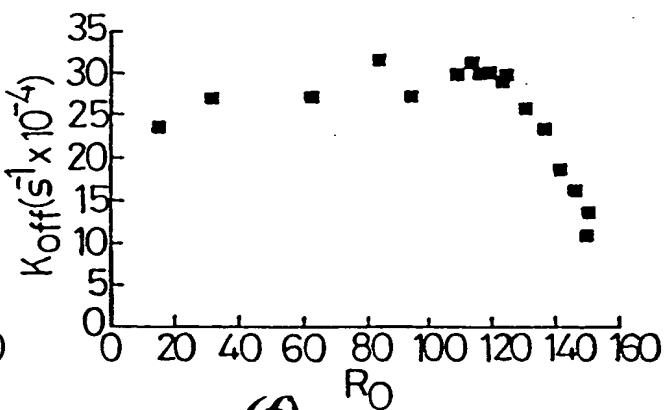
(c)



(d)



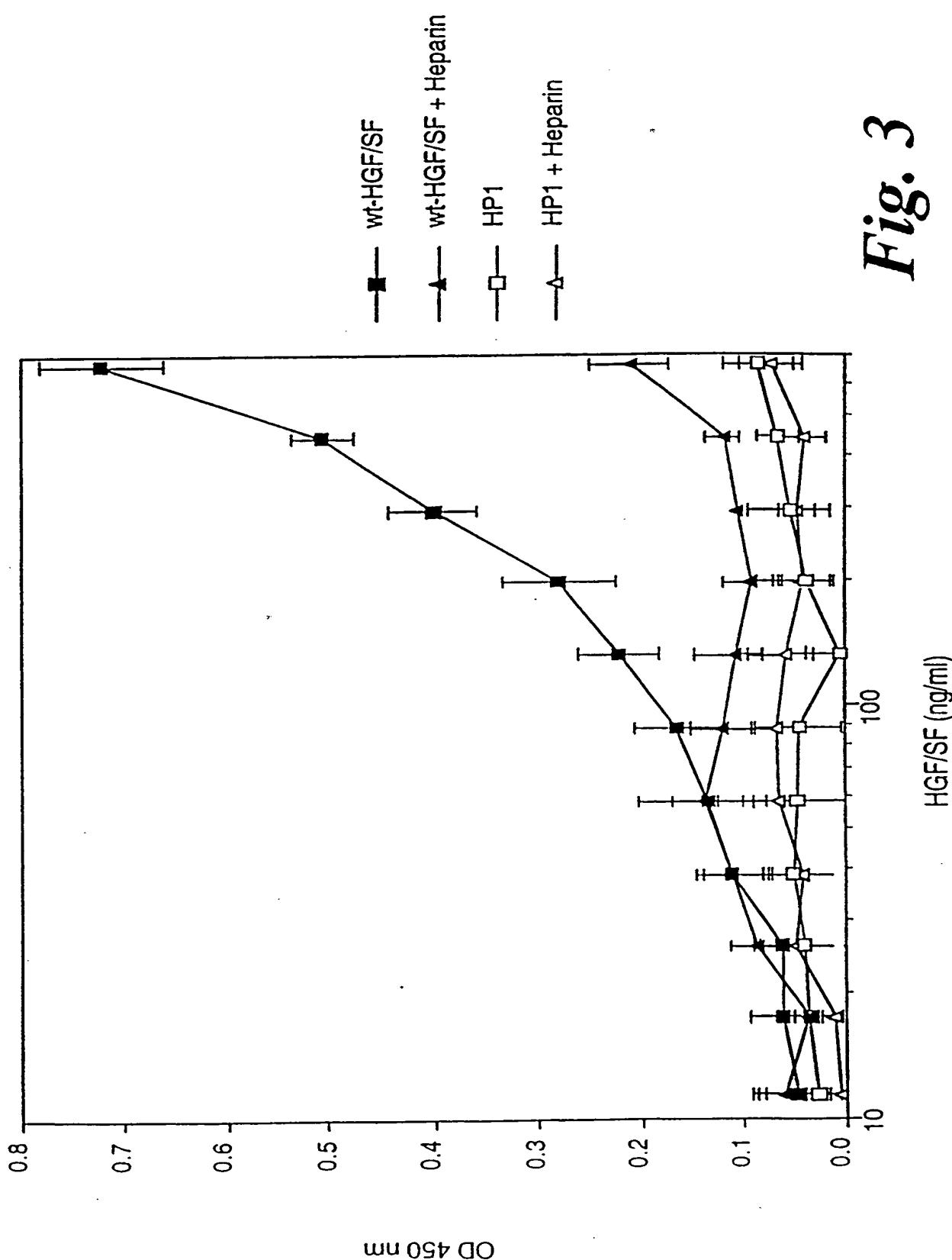
(e)



(f)

Fig. 2

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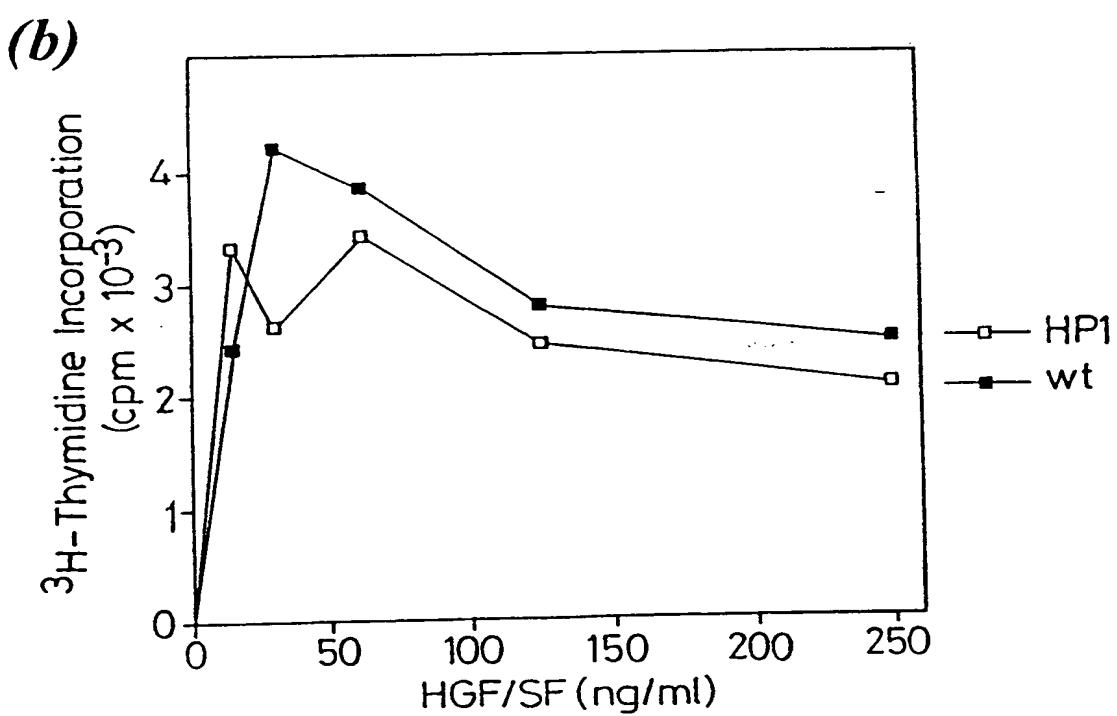
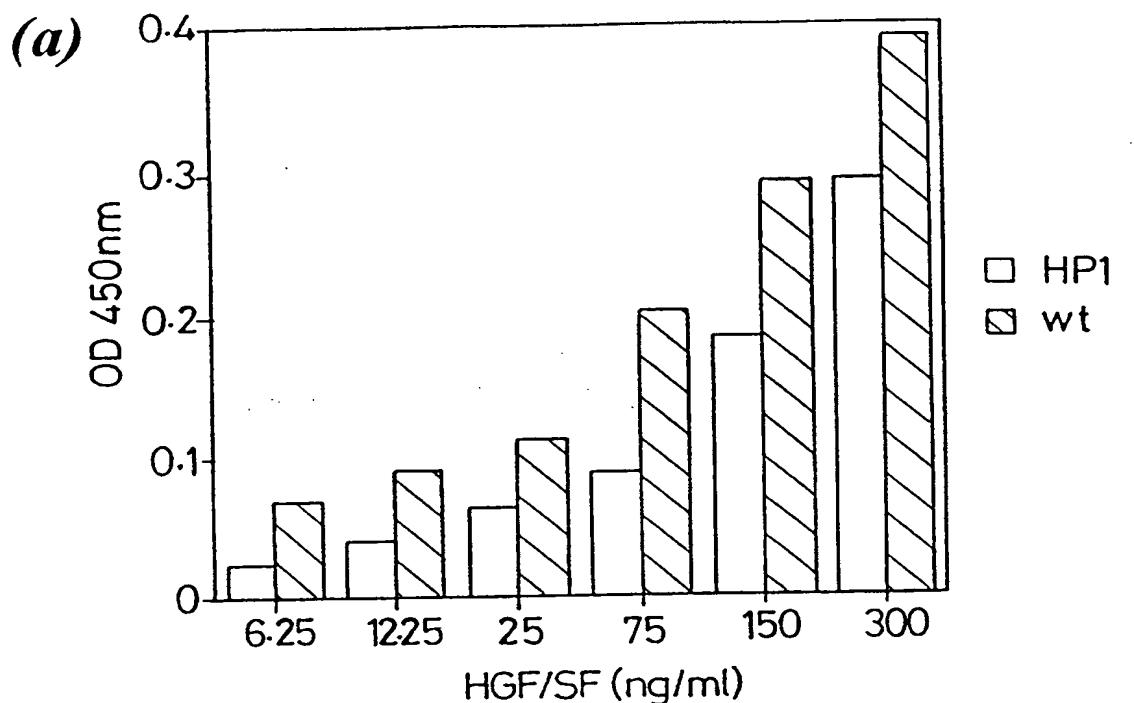


Fig 4

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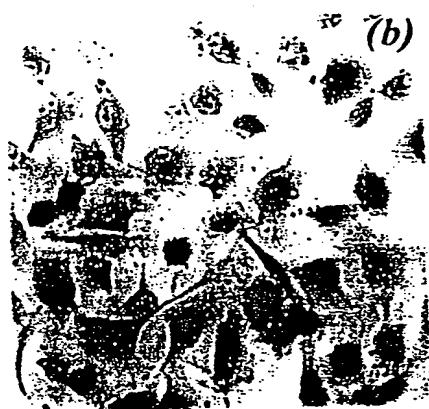
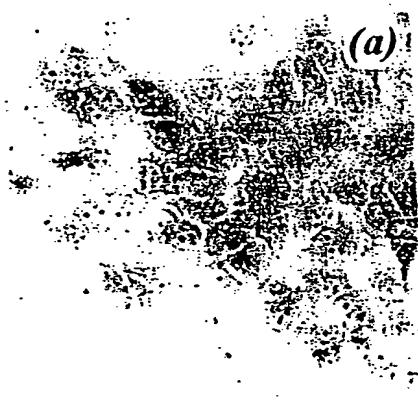


Fig. 5

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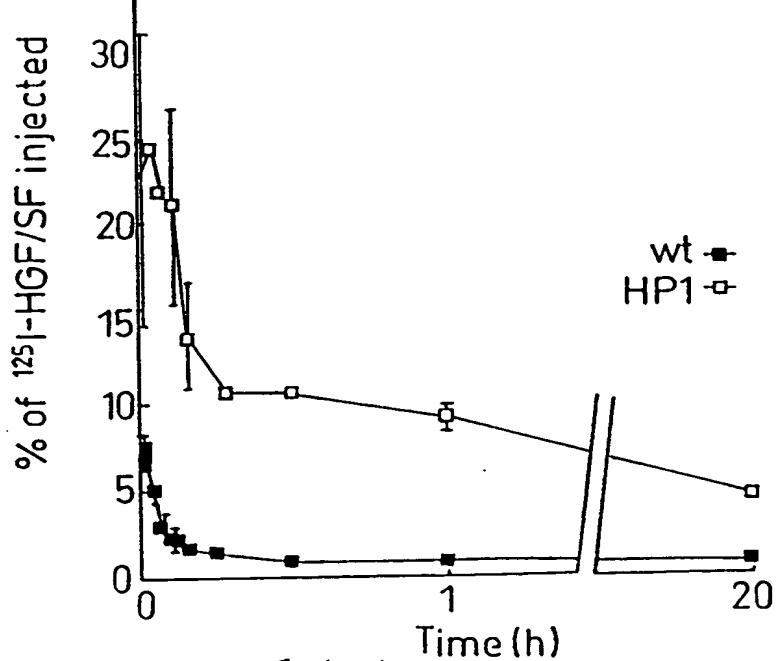


Fig. 6(a)

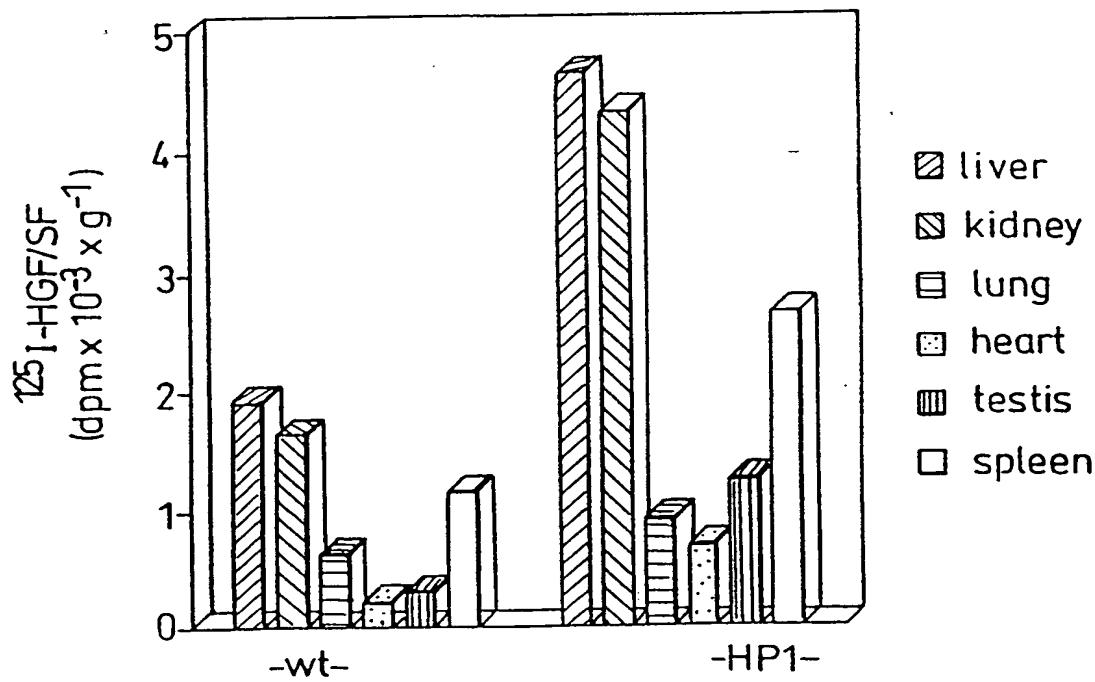


Fig 6(b)

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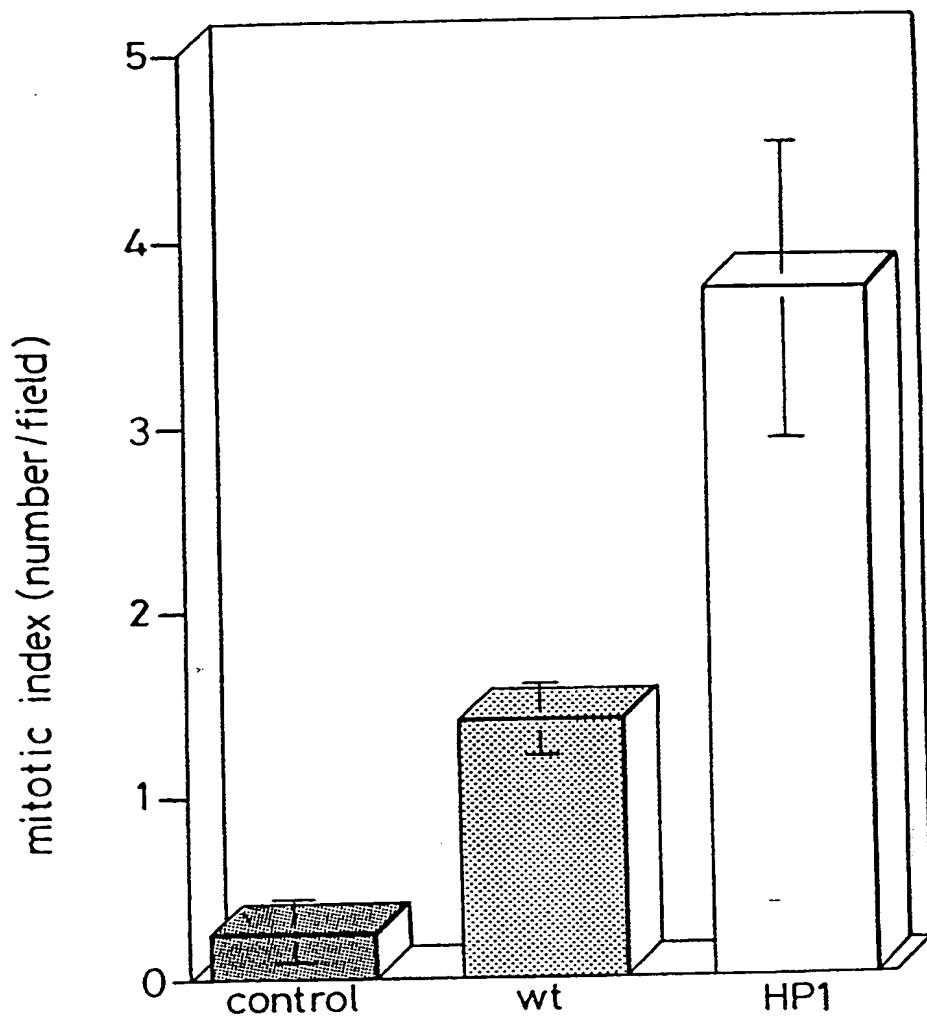


Fig. 6(c)

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HGF_HUMAN (sequence ex SwissProt)

10	20	30	40	50	60
MWVTKLLPAL	LLQHVLLHLL	LLPIAIPYAE	GQRKRRNTIH	EFKKSAKTTL	IKIDPALKIK
70	80	90	100	110	120
TKKVNTADQC	ANRCTRNKGL	PFTCKAFVFD	KARKQCLWFP	FNSMSSGVKK	EFGHEFDLYE
130	140	150	160	170	180
NKDYIRNCII	GKGRSYKGTV	SITKSGIKCQ	PWSSMIPHEH	SFLPSSYRGK	DLQENYCRNP
190	200	210	220	230	240
RGEEGGPWCF	TSNPEVRYEV	CDIPQCSEVE	CMTCNGESYR	GLMDHTESGK	ICQRWDHQTP
250	260	270	280	290	300
HRHKFLPERY	PDKGFDDNYC	RNPDGQPRPW	CYTLDPHTRW	EYCAIKTCAD	NTMNDTDVPL
310	320	330	340	350	360
ETTECIQGQG	EGYRGTVNTI	WNGIPQRWD	SQYPHEHDMT	PENFKCKDLR	ENYCRNPDGS
370	380	390	400	410	420
ESPWCFTTDP	NIRVGYCSQI	PNCDMSHGQD	CYRGNGKNYM	GNLSQTRSGL	TCSMWDKNME
430	440	450	460	470	480
DLHRHIFWEP	DASKLNENYC	RNPDDDAHGP	WCYTGNPLIP	WDYCPISRCE	GDTTPTIVNL
490	500	510	520	530	540
DHPVISCAKT	KQLRVVNGIP	TRTNIGWMVS	LRYRNKHICG	GSLIKESWVL	TARQCFPSRD
550	560	570	580	590	600
LKDYEAWLGI	HDVHGRGDEK	CKQVLNVSQ	VYGPEGSDLV	LMKLARPABL	DDFVSTIDL
610	620	630	640	650	660
NYGCTIPEKT	SCSVYVGWGYT	GLINYDGLLR	VAHLYIMGNE	KCSQHHRGKV	TLNESEICAG
670	680	690	700	710	720
AEKIGSGPCE	GDYGGPLVCE	QHKMRMVLGV	IVPGRGCAIP	NRPGIFVRVA	YYAKWIHKII

LTYKVPQS

Fig. 7